

SEQUENCE LISTING

<110> Novartis AG

<120> ANTIBODY (11C7) ANTI NOGO A AND ITS PHARMACEUTICAL USE

<130> 4-32761P1/UNZ

<140> US/10/538,201

<141> 2006-03-08

<150> PCT/EP03/13960

<151> 2003-12-09

<150> UK 0228832.2

<151> 2002-10-12

<160> 48

<170> PatentIn version 3.5

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> rat NogoA_623-640

<400> 1

Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

<210> 2

<211> 221

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1)..(221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

<400> 2

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30

Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
210 215 220

<210> 3
<211> 238
<212> PRT
<213> Mus musculus

<220>
<221> CHAIN
<222> (1)..(238)
<223> Light Chain of 11C7 with leader sequence

<400> 3

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu
115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 4

<211> 3919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(3579)

<223> Human NogoA

<400>	4		
atg gaa gac ctg gac cag tct cct ctg gtc tcg tcc tcg gac agc cca			48
Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Asp Ser Pro			
1 5 10 15			
ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag			96
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu			
20 25 30			
gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac			144
Asp Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp Glu Asp			
35 40 45			
ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc			192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser			
50 55 60			
gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac			240
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp			
65 70 75 80			
ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc			288
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala			
85 90 95			
gct ccc ccc gtc gcc ccg gag cgg cag ccg tct tgg gac ccg agc ccg			336
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro			
100 105 110			
gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc			384
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val			
115 120 125			
tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc ccg cct ccc			432
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro			
130 135 140			
cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc			480
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr			
145 150 155 160			
ccg cca gcc ccg gct ccc gcc gcg ccc tcc acc ccg gcc gcg ccc			528
Pro Pro Ala Pro Ala Pro Ala Pro Pro Ser Thr Pro Ala Ala Pro			
165 170 175			
aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt			576
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu			
180 185 190			
cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac			624
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp			
195 200 205			
ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc			672
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe			
210 215 220			
cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct			720
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro			
225 230 235 240			
ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca			768
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser			
245 250 255			

aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct	816
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala	
260 265 270	
tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat	864
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp	
275 280 285	
tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc	912
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe	
290 295 300	
agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg	960
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg	
305 310 315 320	
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt	1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser	
325 330 335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa	1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys	
340 345 350	
ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt	1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser	
355 360 365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat	1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr	
370 375 380	
gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag	1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys	
385 390 395 400	
gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg	1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu	
405 410 415	
gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act	1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr	
420 425 430	
aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc	1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro	
435 440 445	
agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt	1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys	
450 455 460	
gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt	1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe	
465 470 475 480	
cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa	1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys	
485 490 495	
ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc	1536
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr	
500 505 510	
aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat	1584

Lys	Thr	Ser	Asn	Pro	Phe	Leu	Val	Ala	Ala	Gln	Asp	Ser	Glu	Thr	Asp	
515							520						525			
tat	gtc	aca	aca	gat	aat	tta	aca	aag	gtg	act	gag	gaa	gtc	gtg	gca	1632
Tyr	Val	Thr	Thr	Asp	Asn	Leu	Thr	Lys	Val	Thr	Glu	Glu	Val	Val	Ala	
530						535					540					
aac	atg	cct	gaa	ggc	ctg	act	cca	gat	tta	gta	cag	gaa	gca	tgt	gaa	1680
Asn	Met	Pro	Glu	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	
545					550					555					560	
agt	gaa	ttg	aat	gaa	gtt	act	ggt	aca	aag	att	gct	tat	gaa	aca	aaa	1728
Ser	Glu	Leu	Asn	Glu	Val	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	
565						570						575				
atg	gac	ttg	gtt	caa	aca	tca	gaa	gtt	atg	caa	gag	tca	ctc	tat	cct	1776
Met	Asp	Leu	Val	Gln	Thr	Ser	Glu	Val	Met	Gln	Glu	Ser	Leu	Tyr	Pro	
580						585						590				
gca	gca	cag	ctt	tgc	cca	tca	ttt	gaa	gag	tca	gaa	gct	act	cct	tca	1824
Ala	Ala	Gln	Leu	Cys	Pro	Ser	Phe	Glu	Glu	Ser	Glu	Ala	Thr	Pro	Ser	
595						600						605				
cca	gtt	ttg	cct	gac	att	gtt	atg	gaa	gca	cca	ttg	aat	tct	gca	gtt	1872
Pro	Val	Leu	Pro	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Ala	Val	
610						615					620					
cct	agt	gct	ggt	gct	tcc	gtg	ata	cag	ccc	agc	tca	tca	cca	tta	gaa	1920
Pro	Ser	Ala	Gly	Ala	Ser	Val	Ile	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	
625						630				635					640	
gct	tct	tca	gtt	aat	tat	gaa	agc	ata	aaa	cat	gag	cct	gaa	aac	ccc	1968
Ala	Ser	Ser	Val	Asn	Tyr	Glu	Ser	Ile	Lys	His	Glu	Pro	Glu	Asn	Pro	
645						650						655				
cca	cca	tat	gaa	gag	gcc	atg	agt	gta	tca	cta	aaa	aaa	gta	tca	gga	2016
Pro	Pro	Tyr	Glu	Glu	Ala	Met	Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	
660						665						670				
ata	aag	gaa	gaa	att	aaa	gag	cct	gaa	aat	att	aat	gca	gct	ctt	caa	2064
Ile	Lys	Glu	Glu	Ile	Lys	Glu	Pro	Glu	Asn	Ile	Asn	Ala	Ala	Leu	Gln	
675						680						685				
gaa	aca	gaa	gct	cct	tat	ata	tct	att	gca	tgt	gat	tta	att	aaa	gaa	2112
Glu	Thr	Glu	Ala	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	
690						695					700					
aca	aag	ctt	tct	gct	gaa	cca	gct	ccg	gat	ttc	tct	gat	tat	tca	gaa	2160
Thr	Lys	Leu	Ser	Ala	Glu	Pro	Ala	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	
705						710				715					720	
atg	gca	aaa	gtt	gaa	cag	cca	gtg	cct	gat	cat	tct	gag	cta	gtt	gaa	2208
Met	Ala	Lys	Val	Glu	Gln	Pro	Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu	
725						730						735				
gat	tcc	tca	cct	gat	tct	gaa	cca	gtt	gac	tta	ttt	agt	gat	gat	tca	2256
Asp	Ser	Ser	Pro	Asp	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	
740						745						750				
ata	cct	gac	gtt	cca	caa	aaa	caa	gat	gaa	act	gtg	atg	ctt	gtg	aaa	2304
Ile	Pro	Asp	Val	Pro	Gln	Lys	Gln	Asp	Glu	Thr	Val	Met	Leu	Val	Lys	
755						760						765				
gaa	agt	ctc	act	gag	act	tca	ttt	gag	tca	atg	ata	gaa	tat	gaa	aat	2352
Glu	Ser	Leu	Thr	Glu	Thr	Ser	Phe	Glu	Ser	Met	Ile	Glu	Tyr	Glu	Asn	

770	775	780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu 785 790 795 800			2400
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro 805 810 815			2448
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met 820 825 830			2496
gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser 835 840 845			2544
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro 850 855 860			2592
att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp 865 870 875 880			2640
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His 885 890 895			2688
aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys 900 905 910			2736
aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val 915 920 925			2784
gaa gag aaa atc agt ttc tca gat gac ttt tct aaa aat ggg tct gct Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala 930 935 940			2832
aca tca aag gtg ctc tta ttg cct cca gat gtt tct gct ttg gcc act Thr Ser Lys Val Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr 945 950 955 960			2880
caa gca gag ata gag agc ata gtt aaa ccc aaa gtt ctt gtg aaa gaa Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu 965 970 975			2928
gct gag aaa aaa ctt cct tcc gat aca gaa aaa gag gac aga tca cca Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro 980 985 990			2976
tct gct ata ttt tca gca gag ctg agt aaa act tca gtt gtt gac ctc Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu 995 1000 1005			3024
ctg tac tgg aga gac att aag aag act gga gtg gtg ttt ggt gcc Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala 1010 1015 1020			3069
agc cta ttc ctg ctg ctt tca ttg aca gta ttc agc att gtg agc Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser 1025 1030 1035			3114

gta aca gcc tac att gcc ttg	1040	gca ctg ctc tct gtg	1045	acc atc agc	3159
Val Thr Ala Tyr Ile Ala Leu		Ala Leu Leu Ser Val		Thr Ile Ser	
ttt agg ata tac aag ggt gtg	1055	atc caa gct atc cag	1060	aaa tca gat	3204
Phe Arg Ile Tyr Lys Gly Val		Ile Gln Ala Ile Gln		Lys Ser Asp	
gaa ggc cac cca ttc agg gca	1070	tat ctg gaa tct gaa	1075	gtt gct ata	3249
Glu Gly His Pro Phe Arg Ala		Tyr Leu Glu Ser Glu		Val Ala Ile	
tct gag gag ttg gtt cag aag	1085	tac agt aat tct gct	1090	ctt ggt cat	3294
Ser Glu Glu Leu Val Gln Lys		Tyr Ser Asn Ser Ala		Leu Gly His	
gtg aac tgc acg ata aag gaa	1100	ctc agg cgc ctc ttc	1105	tta gtt gat	3339
Val Asn Cys Thr Ile Lys Glu		Leu Arg Arg Leu Phe		Leu Val Asp	
gat tta gtt gat tct ctg aag	1115	ttt gca gtg ttg atg	1120	tgg gta ttt	3384
Asp Leu Val Asp Ser Leu Lys		Phe Ala Val Leu Met		Trp Val Phe	
acc tat gtt ggt gcc ttg ttt	1130	aat ggt ctg aca cta	1135	ctg att ttg	3429
Thr Tyr Val Gly Ala Leu Phe		Asn Gly Leu Thr Leu		Leu Ile Leu	
gct ctc att tca ctc ttc agt	1145	gtt cct gtt att tat	1150	gaa cgg cat	3474
Ala Leu Ile Ser Leu Phe Ser		Val Pro Val Ile Tyr		Glu Arg His	
cag gca cag ata gat cat tat	1160	cta gga ctt gca aat	1165	aag aat gtt	3519
Gln Ala Gln Ile Asp His Tyr		Leu Gly Leu Ala Asn		Lys Asn Val	
aaa gat gct atg gct aaa atc	1175	1170			
Lys Asp Ala Met Ala Lys Ile		caa gca aaa atc cct	1180	aat gga ttg aag	3564
cgc aaa gct gaa tga aaacgcccaa aataattagt aggagttcat cttaaaggg		1185			3619
Arg Lys Ala Glu	1190				
gatattcatt tgattatacg ggggagggtc agggagaac gAACCTGAC gttgcagtgc					3679
agtttcacag atcggttta gatctttatt tttagccatg cactgttgcg aggaaaaatt					3739
acctgtctt actgccatgt gttcatcatc ttaagtattg taagctgcta tgtatggatt					3799
taaaccgtaa tcatatctt ttcctatctg aggcactggt ggaataaaaa acctgtatat					3859
tttactttgt tgcagatagt cttgccat cttggcaagt tgcagagatg gtggagctag					3919

<210> 5
 <211> 1192
 <212> PRT
 <213> Homo sapiens

<400> 5

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
 1 5 10 15

Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30

Asp Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu
405 410 415

Glu Ser Lys Val Asp Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
420 425 430

Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
435 440 445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
450 455 460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
465 470 475 480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
485 490 495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
500 505 510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp
515 520 525

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
530 535 540

Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
545 550 555 560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu

785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu
995 1000 1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala
1010 1015 1020

Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
1025 1030 1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
1040 1045 1050

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
1175 1180 1185

Arg Lys Ala Glu
1190

<210> 6
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Human NogoA_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

<210> 7
<211> 819

<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(819)
<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg
1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile
20 25 30

Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val
305 310 315 320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
355 360 365

Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
370 375 380

Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
385 390 395 400

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
405 410 415

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
420 425 430

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
435 440 445

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
450 455 460

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
805 810 815

Lys Thr Ser

<210> 8
<211> 10
<212> PRT
<213> Mus musculus

<220>
<221> BINDING
<222> (1)..(10)
<223> hypervariable part of heavy chain of 11C7

<400> 8

Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
1 5 10

<210> 9
<211> 17
<212> PRT
<213> Mus musculus

<220>
<221> BINDING
<222> (1)..(17)
<223> hypervariable part of heavy chain of 11C7

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 10
<211> 9
<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of heavy chain of 11C7

<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr
1 5

<210> 11

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(16)

<223> hypervariable part of light chain of 11C7

<400> 11

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 13

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of light chain of 11C7

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr
1 5

<210> 14
<211> 30
<212> DNA
<213> *Mus musculus*

<220>
<221> misc_binding
<222> (1)..(30)
<223> DNA-CDR1-11C7

<400> 14
ggattcgatt ttagaagaaa ttggatgagt 30

<210> 15
<211> 51
<212> DNA
<213> *Mus musculus*

<220>
<221> misc_binding
<222> (1)..(51)
<223> DNA-CDR2-11C7

<400> 15
gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> 16
<211> 27
<212> DNA
<213> *Mus musculus*

<220>
<221> misc_binding
<222> (1)..(27)
<223> DNA-CDR3-11C7

<400> 16
ccggtctgga tgtatgctat ggactac 27

<210> 17
<211> 48
<212> DNA
<213> *Mus musculus*

<220>
<221> misc_binding
<222> (1)..(48)
<223> DNA-CDR'1-11C7

<400> 17
aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat 48

<210> 18
<211> 21
<212> DNA
<213> *Mus musculus*

<220>
 <221> misc_binding
 <222> (1)..(21)
 <223> DNA-CDR'2-11C7

<400> 18
 ctggtgtcta aactggactc t 21

<210> 19
 <211> 27
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_binding
 <222> (1)..(27)
 <223> DNA-CDR'3-11C7

<400> 19
 tggcaaggta cacatttcc tcagacg 27

<210> 20
 <211> 54
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(54)
 <223> Leader sequence for heavy chain of 11C7

<400> 20
 atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
 1 5 10 15

cag tgt 54
 Gln Cys

<210> 21
 <211> 18
 <212> PRT
 <213> Mus musculus

<400> 21
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
 1 5 10 15

Gln Cys

<210> 22
 <211> 57
 <212> DNA
 <213> Mus musculus

<220>
<221> CDS
<222> (1)..(57)
<223> Leader sequence for 11C7-light chain

<400> 22
atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cg⁴⁸
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

acc agc ggt
Thr Ser Gly 57

<210> 23
<211> 19
<212> PRT
<213> Mus musculus

<400> 23
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly

<210> 24
<211> 181
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(181)
<223> human Nig-D20

<400> 24
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
115 120 125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
130 135 140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
145 150 155 160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
165 170 175

Pro Val Asp Leu Phe
180

<210> 25
<211> 3492
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(3492)
<223> rat NogoA

<400> 25
atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc acg gac agc 48
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc 96
Pro Pro Arg Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
20 25 30

gag gac gag gag gac gag gag gag gac gag gag gag gac gag 144
Glu Asp Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcg ccg ctg ctg gac 240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc 288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc 336

Ala	Pro	Pro	Ala	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Glu	Arg	Ser	Pro	
100						105						110				
gcg	gcg	ccc	gcg	cca	tcc	ctg	ccg	ccc	gct	gcc	gca	gtc	ctg	ccc	tcc	384
Ala	Ala	Pro	Ala	Pro	Ser	Leu	Pro	Pro	Ala	Ala	Ala	Val	Leu	Pro	Ser	
115						120						125				
aag	ctc	cca	gag	gac	gac	gag	cct	ccg	gcg	agg	ccc	ccg	cct	ccg	ccg	432
Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro	Pro	Pro	Pro	
130						135					140					
cca	gcc	ggc	gcg	agc	ccc	ctg	gcg	gag	ccc	gcc	gcg	ccc	cct	tcc	acg	480
Pro	Ala	Gly	Ala	Ser	Pro	Leu	Ala	Glu	Pro	Ala	Ala	Pro	Pro	Ser	Thr	
145						150					155					
ccg	gcc	gcf	ccc	aag	cgc	agg	ggc	tcc	ggc	tca	gtg	gat	gag	acc	ctt	528
Pro	Ala	Ala	Pro	Lys	Arg	Arg	Gly	Ser	Gly	Ser	Val	Asp	Glu	Thr	Leu	
165						170					175					
ttt	gct	ctt	cct	gct	gca	tct	gag	cct	gtg	ata	ccc	tcc	tct	gca	gaa	576
Phe	Ala	Leu	Pro	Ala	Ala	Ser	Glu	Pro	Val	Ile	Pro	Ser	Ser	Ala	Glu	
180						185					190					
aaa	att	atg	gat	ttg	atg	gag	cag	cca	ggt	aac	act	gtt	tcg	tct	ggt	624
Lys	Ile	Met	Asp	Leu	Met	Glu	Gln	Pro	Gly	Asn	Thr	Val	Ser	Ser	Gly	
195						200					205					
caa	gag	gat	tcc	cca	tct	gtc	ctg	ctt	gaa	act	gct	gcc	tct	ctt	cct	672
Gln	Glu	Asp	Phe	Pro	Ser	Val	Leu	Leu	Glu	Thr	Ala	Ala	Ser	Leu	Pro	
210						215					220					
tct	cta	tct	ctc	tca	act	gtt	tct	ttt	aaa	gaa	cat	gga	tac	ctt		720
Ser	Leu	Ser	Pro	Leu	Ser	Thr	Val	Ser	Phe	Lys	Glu	His	Gly	Tyr	Leu	
225						230					235					
ggt	aac	tta	tca	gca	gtg	tca	tcc	tca	gaa	gga	aca	att	gaa	gaa	act	768
Gly	Asn	Leu	Ser	Ala	Val	Ser	Ser	Ser	Glu	Gly	Thr	Ile	Glu	Glu	Thr	
245						250					255					
tta	aat	gaa	gct	tct	aaa	gag	ttg	cca	gag	agg	gca	aca	aat	cca	ttt	816
Leu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Pro	Glu	Arg	Ala	Thr	Asn	Pro	Phe	
260						265					270					
gta	aat	aga	gat	tta	gca	gaa	ttt	tca	gaa	tta	gaa	tat	tca	gaa	atg	864
Val	Asn	Arg	Asp	Leu	Ala	Glu	Phe	Ser	Glu	Leu	Glu	Tyr	Ser	Glu	Met	
275						280					285					
gga	tca	tct	ttt	aaa	ggc	tcc	cca	aaa	gga	gag	tca	gcc	ata	tta	gta	912
Gly	Ser	Ser	Phe	Lys	Gly	Ser	Pro	Lys	Gly	Glu	Ser	Ala	Ile	Leu	Val	
290						295					300					
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu	Val	Ile	Val	Arg	Ser	Lys	Asp	Lys	Glu	Asp	
305						310					315					
tta	gtt	tgt	agt	gca	gcc	ctt	cac	agt	cca	caa	gaa	tca	cct	gtg	ggt	1008
Leu	Val	Cys	Ser	Ala	Ala	Leu	His	Ser	Pro	Gln	Glu	Ser	Pro	Val	Gly	
325						330					335					
aaa	gaa	gac	aga	gtt	gtg	tct	cca	gaa	aag	aca	atg	gac	att	ttt	aat	1056
Lys	Glu	Asp	Arg	Val	Val	Ser	Pro	Glu	Lys	Thr	Met	Asp	Ile	Phe	Asn	
340						345					350					
gaa	atg	cag	atg	tca	gta	gta	gca	cct	gtg	agg	gaa	gag	tat	gca	gac	1104
Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	Tyr	Ala	Asp	

	355	360	365	
ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga				1152
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly				
370 375 380				
agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac				1200
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp				
385 390 395 400				
aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat				1248
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp				
405 410 415				
agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct				1296
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro				
420 425 430				
gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca				1344
Val Lys Asp Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser				
435 440 445				
gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat				1392
Ala Thr Glu Ser Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His				
450 455 460				
act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc				1440
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala				
465 470 475 480				
caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt				1488
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu				
485 490 495				
gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta				1536
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu				
500 505 510				
tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg				1584
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr				
515 520 525				
cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca				1632
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr				
530 535 540				
ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca				1680
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser				
545 550 555 560				
gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca				1728
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser				
565 570 575				
ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt				1776
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val				
580 585 590				
atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta				1824
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val				
595 600 605				
gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat				1872
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr				
610 615 620				

gac	agt	ata	aag	ctt	gag	cct	gaa	aac	ccc	cca	cca	tat	gaa	gaa	gcc	1920
Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	
625				630					635						640	
atg	aat	gta	gca	cta	aaa	gct	ttg	gga	aca	aag	gaa	gga	ata	aaa	gag	1968
Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	Ile	Lys	Glu	
				645					650					655		
cct	gaa	agt	ttt	aat	gca	gct	gtt	cag	gaa	aca	gaa	gct	cct	tat	ata	2016
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile	
				660				665					670			
tcc	att	gcg	tgt	gat	tta	att	aaa	gaa	aca	aag	ctc	tcc	act	gag	cca	2064
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro	
				675				680					685			
agt	cca	gat	ttc	tct	aat	tat	tca	gaa	ata	gca	aaa	ttc	gag	aag	tcg	2112
Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	Glu	Lys	Ser	
				690				695				700				
gtg	ccc	gaa	cac	gct	gag	cta	gtg	gag	gat	tcc	tca	cct	gaa	tct	gaa	2160
Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Glu	Ser	Glu	
				705				710				715			720	
cca	gtt	gac	tta	ttt	agt	gat	gat	tcg	att	cct	gaa	gtc	cca	caa	aca	2208
Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	Pro	Gln	Thr	
				725				730					735			
caa	gag	gag	gct	gtg	atg	ctc	atg	aag	gag	agt	ctc	act	gaa	gtg	tct	2256
Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	Glu	Val	Ser	
				740				745					750			
gag	aca	gta	gcc	cag	cac	aaa	gag	gag	aga	ctt	agt	gcc	tca	cct	cag	2304
Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala	Ser	Pro	Gln	
				755				760				765				
gag	cta	gga	aag	cca	tat	tta	gag	tct	ttt	cag	ccc	aat	tta	cat	agt	2352
Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro	Asn	Leu	His	Ser	
				770				775				780				
aca	aaa	gat	gct	gca	tct	aat	gac	att	cca	aca	ttg	acc	aaa	aag	gag	2400
Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	Lys	Lys	Glu	
				785				790				795			800	
aaa	att	tct	ttg	caa	atg	gaa	gag	ttt	aat	act	gca	att	tat	tca	aat	2448
Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	Tyr	Ser	Asn	
				805				810				815				
gat	gac	tta	ctt	tct	tct	aag	gaa	gac	aaa	ata	aaa	gaa	agt	gaa	aca	2496
Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	Ser	Glu	Thr	
				820				825				830				
ttt	tca	gat	tca	tct	ccg	att	gag	ata	ata	gat	gaa	ttt	ccc	acg	ttt	2544
Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Phe	
				835				840				845				
gtc	agt	gct	aaa	gat	gat	tct	cct	aaa	tta	gcc	aag	gag	tac	act	gat	2592
Val	Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu	Tyr	Thr	Asp	
				850				855				860				
cta	gaa	gta	tcc	gac	aaa	agt	gaa	att	gct	aat	atc	caa	agc	ggg	gca	2640
Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	Ser	Gly	Ala	
				865				870				875			880	

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat	2688
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Ash	
885 890 895	
ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat	2736
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn	
900 905 910	
agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct	2784
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala	
915 920 925	
ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt	2832
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu	
930 935 940	
acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac	2880
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp	
945 950 955 960	
aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt	2928
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val	
965 970 975	
gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt	2976
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe	
980 985 990	
ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc	3024
Gly Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val	
995 1000 1005	
agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc	3069
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile	
1010 1015 1020	
agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca	3114
Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	
1025 1030 1035	
gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	3159
Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	
1040 1045 1050	
ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt	3204
Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly	
1055 1060 1065	
cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt	3249
His Val Asn Ser Thr Ile Lys 1070 1075	
1080	
1085 1090 1095	
gat gat tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg	3294
Asp Asp Leu Val Asp Ser Leu 1100 1105	
1110	
ttt act tat gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att	3339
Phe Thr Tyr Val Gly Ala Leu 1115 1120	
1125	
tta gct ctg atc tca ctc ttc agt att cct gtt att tat gaa cgg	3384
Leu Ala Leu Ile Ser Leu Phe 1115 1120	
1125	
cat cag gtg cag ata gat cat tat cta gga ctt gca aac aag agt	3429

His Gln Val Gln Ile Asp His	1130	Tyr Leu Gly Leu Ala	1135	Asn Lys Ser	1140		
gtt aag gat gcc atg gcc		aaa atc caa gca		aaa atc cct gga	ttg	3474	
Val Lys Asp Ala Met Ala	1145	Lys Ile Gln Ala Lys	1150	Ile Pro Gly Leu	1155		
aag cgc aaa gca gat tga						3492	
Lys Arg Lys Ala Asp	1160						
<210> 26							
<211> 1163							
<212> PRT							
<213> Rattus norvegicus							
<400> 26							
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser	1	5	10	15			
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro	20	25	30				
Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp	35	40	45				
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly	50	55	60				
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp	65	70	75	80			
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala	85	90	95				
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro	100	105	110				
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser	115	120	125				
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro	130	135	140				
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr	145	150	155	160			
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu	165	170	175				
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu	180	185	190				

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
370 375 380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385 390 395 400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
405 410 415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
420 425 430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705 710 715 720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
725 730 735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
740 745 750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
755 760 765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
770 775 780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785 790 795 800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
805 810 815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
835 840 845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

<210> 27
<211> 25
<212> PRT
<213> Rattus norvegicus

<220>
<221> PEPTIDE
<222> (1)...(25)
<223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer_bind

<222> (1)..(28)

<400> 30
aactgcagta ctgagctcct ccatctgc 28

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> forward 5'

<220>
<221> primer_bind
<222> (1)..(33)
<223> forward primer

<400> 31
gtcgccgatc catggagacc cttttgctc ttc 33

<210> 32
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse 5'

<220>
<221> primer_bind
<222> (1)..(27)
<223> reverse primer

<400> 32
gttctcgagt tatgaagttt tactcag 27

<210> 33
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> forward 5'-1

<220>
<221> primer_bind
<222> (1)..(29)
<223> primer

<400> 33
gtgcggatcc atggatttga aggagcagc 29

<210> 34
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>
<221> primer_bind
<222> (1)..(28)
<223> primer

<400> 34
gtttctcgag tgaagttta ttcagctc

28

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer

<220>
<221> primer_bind
<222> (1)..(20)
<223> primer

<400> 35
tccaccccg ccgcgccaa

20

<210> 36
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' primer 2

<220>
<221> primer_bind
<222> (1)..(22)
<223> primer

<400> 36
aatgatgggc aaagctgtgc tg

22

<210> 37
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' primer

<220>
<221> primer_bind
<222> (1)..(24)
<223> primer

<400> 37
ggtacaaaga ttgcttatga aaca

24

<210> 38
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> primer_bind
<222> (1)..(22)
<223> primer

<400> 38
aggcaatgta gg 22

<210> 39
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'-VL leader

<220>
<221> primer_bind
<222> (1)..(28)
<223> primer

<400> 39
aatatgagtc ctgcccagtt cctgttcc 28

<210> 40
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> 3'-Ck

<220>
<221> primer_bind
<222> (1)..(32)
<223> primer

<400> 40
tttaggaattc ctaacactct cccctgttga ag 32

<210> 41
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 5'-VH leader

<220>

```

<221> primer_bind
<222> (1)..(31)
<223> primer

<400> 41
aatatggatt ttgggctgat ttttttatt g 31

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> 3'-CH hinge

<220>
<221> primer_bind
<222> (1)..(24)
<223> primer

<400> 42
aattgggcaa cgttgcaggt gacg 24

<210> 43
<211> 663
<212> DNA
<213> Mus musculus

<220>
<221> misc_binding
<222> (1)..(663)
<223> DNA variable part of heavy chain 11C7

<400> 43
atggattttg ggctgatttt ttttattgtt ggtcttttaa aagggttcca gtgtgaggtg 60
aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120
gtagtcctcg gattcgattt tagaagaat tggatgagtt gggtccggca ggctcctgg 180
aaaggcttag aatggattgg agaaattaaat ccagatagca gtaagataaa ctatacgcca 240
tctctaaagg ataaattcat catctccaga gacaatgccca agaatacgct gtacctgca 300
gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360
tatgctatgg actactgggg tcaaggaacc tcagtcaccc tctcctcgca caaaacgaca 420
cccccatctg tctatccact ggccccctgga tctgctgccc aaactaactc catggtgacc 480
ctgggatgcc tggtcaaggg ctattccct gagccagtgca cagtgacctg gaactctgga 540
tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgaccc ctacactctg 600
agcagctcag tgactgtccc ctccagcacc tggcccagcg agaccgtcac ctgcaacggtt 660
gcc 663

<210> 44
<211> 717

```

<212> DNA
<213> Mus musculus

<220>
<221> misc_binding
<222> (1)..(717)
<223> variable part of light chain of 11c7

<400> 44
atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcggaaac cagcggtat 60
gttctgttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc 120
tcttgcaagt caagtcagag cctcttgcatt agtgatggaa agacatattt gaattggttg 180
ttacagaggc caggccagtc tccaaagcgc ctaatctatc tgggtctaa actggactct 240
ggagttccctg acaggttacac tggcagtggta tcagggacgg atttcacact gaaaatcagc 300
agagtgaggc ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag 360
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420
atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480
aacaacttct accccaaaga catcaatgtc aagtggaaaga ttgatggcag tgaacgacaa 540
aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600
agcaccctca cgttgaccaa ggacgagttt gaacgacata acagctatac ctgtgaggcc 660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717

<210> 45
<211> 239
<212> PRT
<213> Homo sapiens

<400> 45

Thr Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
85 90 95

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220

Gln Asp Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr
225 230 235

<210> 46
<211> 239
<212> PRT
<213> Pan paniscus

<400> 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala

85

90

95

Val Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
100 105 110

Ser Ile Ile His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
115 120 125

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
130 135 140

Pro Glu Ser Ile Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
165 170 175

Thr Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
180 185 190

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys
210 215 220

Gln Asp Glu Ala Val Met Leu Val Lys Glu Asn Leu Pro Glu Thr
225 230 235

<210> 47
<211> 239
<212> PRT
<213> Rattus norvegicus

<400> 47

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
35 40 45

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
85 90 95

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
100 105 110

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
115 120 125

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
130 135 140

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
165 170 175

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
180 185 190

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
210 215 220

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val
225 230 235

<210> 48

<211> 239

<212> PRT

<213> Mus musculus

<400> 48

Ser Lys Val Thr Glu Ala Val Val Ala Thr Met Pro Glu Gly Leu Thr
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
35 40 45

Glu Ala Ile Gln Glu Ser Ile Tyr Pro Thr Ala Gln Leu Cys Pro Ser
50 55 60

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val

65

70

75

80

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Thr Gly Ala Ser Val
85 90 95

Ala Gln Pro Ser Ala Ser Pro Leu Glu Val Pro Ser Pro Val Ser Tyr
100 105 110

Asp Gly Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
115 120 125

Met Ser Val Ala Leu Lys Thr Ser Asp Ser Lys Glu Glu Ile Lys Glu
130 135 140

Pro Glu Ser Phe Asn Ala Ala Ala Gln Glu Ala Glu Ala Pro Tyr Ile
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
165 170 175

Ser Pro Glu Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
180 185 190

Val Pro Asp His Cys Glu Leu Val Asp Asp Ser Ser Pro Glu Ser Glu
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
210 215 220

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val
225 230 235